

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1-22. (cancelled)

23. (currently amended) A purified HIV-1 variant virus,

wherein said HIV-1 variant virus differs at the amino acid sequence level from HIV-1_{BRU} by from 9.8 to 12% in the entire Gag protein, from 5.5 to 7.7% in the entire Pol protein, and 20.7 to 21.7% in the entire Env protein ~~the group of viruses consisting of HIV-1_{III_B}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in the entire Pol protein, and 13.0% in the entire Env protein,~~

wherein the HIV-1 variant virus binds antibodies in AIDS patient sera ~~bind to~~ Gag, Pol, or Env polypeptides of said HIV-1 variant virus,

~~wherein said antibodies bind to Gag, Pol, or Env polypeptides of~~ binding specifically to the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641,

wherein the genetic structure of said HIV-1 variant is 5'-LTR-gag-pol-vif-vpr-tat-rev-vpu-env-nef-LTR-3', and

wherein the nucleic acid of said HIV-1 variant virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of HIV-1_{MAL}.

24. (cancelled)

25. (previously presented) The HIV-1 variant virus of claim 23, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a DNA probe comprising a restriction enzyme fragment of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

26-42. (cancelled)

43. (previously presented) The HIV-1 variant virus of claim 23, wherein said HIV-1 variant virus differs genetically from HIV-1_{MAL} by 0-10.8% in Gag, 0%-8.4% in Pol, and 0%-19.8% in Env.

44. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Env sequence of HIV-1_{MAL} as shown in Figure 3.

45. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Gag sequence of HIV-1_{MAL} as shown in Figure 3.

46. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Pol sequence of HIV-1_{MAL} as shown in Figure 3.

47. (cancelled)

48. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus differs at the amino acid sequence level from HIV-1_{BRU} by
from 9.8 to 12% in the entire Gag protein, from 5.5 to 7.7% in the entire Pol protein,
and 20.7 to 21.7% in the entire Env protein ~~the group of viruses consisting of HIV-~~
~~1_{HIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in~~
~~the entire Pol protein, and 13.0% in the entire Env protein;~~

the HIV-1 variant virus binds antibodies in AIDS patient sera ~~bind to Gag, Pol,~~
~~or Env polypeptides of said LAV_{MAL} virus;~~

said antibodies ~~bind to Gag, Pol, or Env polypeptides of~~ binding specifically to
the virus deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5'-LTR-gag-pol-vif-vpr-tat-rev-
vpu-env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent
hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe
comprising the genomic cDNA of the virus deposited at the COLLECTION
NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No.
I-641; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the
restriction map shown in Fig. 1.

49. (previously presented) The purified human immunodeficiency virus designated LAV_{MAL} of claim 48, wherein the genome of LAV_{MAL} has the restriction map shown in Fig. 1.

50. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus differs at the amino acid sequence level from HIV-1_{BRU} by
from 9.8 to 12% in the entire Gag protein, from 5.5 to 7.7% in the entire Pol protein,
and 20.7 to 21.7% in the entire Env protein ~~the group of viruses consisting of HIV-~~
~~1_{IIIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in~~
~~the entire Pol protein, and 13.0% in the entire Env protein;~~

the HIV-1 variant virus binds antibodies in AIDS patient sera ~~bind to Gag, Pol,~~
~~or Env polypeptides of said LAV_{MAL} virus;~~

said antibodies ~~bind to Gag, Pol, or Env polypeptides of~~ binding specifically to
the virus deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-*
env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent
hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe
comprising the genomic cDNA of the virus deposited at the COLLECTION
NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No.

I-641; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 1 to 530; 34-530; and 531-877.

51. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus differs at the amino acid sequence level from HIV-1_{BRU} by
from 9.8 to 12% in the entire Gag protein, from 5.5 to 7.7% in the entire Pol protein,
and 20.7 to 21.7% in the entire Env protein ~~the group of viruses consisting of HIV-~~
~~1_{IIIIB}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in~~
~~the entire Pol protein, and 13.0% in the entire Env protein;~~

the HIV-1 variant virus binds antibodies in AIDS patient sera ~~bind to Gag, Pol,~~
~~or Env polypeptides of said LAV_{MAL} virus;~~

said antibodies ~~bind to Gag, Pol, or Env polypeptides of~~ binding specifically to
the virus deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-*
env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent
hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe

comprising the genomic cDNA of the virus deposited at the COLLECTION
NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No.
I-641; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least
one of the following LAV_{MAL} cDNA sequences of Fig 3E: 37-130, 211-289, 488-530,
490-620, and 680-700.

52. (currently amended) A purified human immunodeficiency virus
designated LAV_{MAL}, wherein

said LAV_{MAL} virus differs at the amino acid sequence level from HIV-1_{BRU} by
from 9.8 to 12% in the entire Gag protein, from 5.5 to 7.7% in the entire Pol protein,
and 20.7 to 21.7% in the entire Env protein ~~the group of viruses consisting of HIV-~~
~~1_{IIIb}, HIV-1_{BRU}, and HIV-1_{ARV-2} greater than 3.4% in the entire Gag protein, 3.1% in~~
~~the entire Pol protein, and 13.0% in the entire Env protein;~~

the HIV-1 variant virus binds antibodies in AIDS patient sera ~~bind to Gag, Pol,~~
~~or Env polypeptides of said LAV_{MAL} virus;~~

said antibodies ~~bind to Gag, Pol, or Env polypeptides of~~ binding specifically to
the virus deposited at the COLLECTION NATIONALE DES CULTURES DE
MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-*
env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641, or a restriction enzyme fragment thereof, wherein the restriction enzyme is selected from at least one of the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the restriction map shown in Fig. 1.